SEQUENCE

SEQ ID NO: 1

Sequence Length: 780

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: cDNA

Seque	enc	ce		:												
TGGTGAAGCT CTAACGGCTG TTTTGACTGG CGTAGCCGGA GCCGGCGACG TGAGGCGGGC											60					
												114				
			`	' /		1				Met	Glu	Gly	Cys	Val	Ser	
						/ /				1				5		
AAC C	TA	ATG	GTC	TGC	AAC	ETG	GCC	TAC	AGC	GGG	AAG	CTG	GAA	GAG	TTG	162
Asn L	eu	Met	Val	Cys	Asn	Len	Ala	Tyr	Ser	Gly	Lys	Leu	Glu	Glu	Leu	
			10		1	$\setminus \setminus$		15					20			
AAG G	AG	AGT	TTA	CTG	gcc/	фAT	AAA	TCC	CTG	GCT	ACT	AGA	ACT	GAC	CAG	210
Lys G	lu	Ser	Ile	Leu	Ala	Asp	__ Lys	Ser	Leu	Ala	Thr	Arg	Thr	Asp	Gln	
		25					\30					35				
GAC A	.GC	AGA	ACT	GCA	TTG	CAC	TGG	GCÀ	TGC	TCA	GCT	GGA	CAT	ACA	GAA	258
Asp S	er	Arg	Thr	Ala	Leu	His	Trp	Ala	çÃa	Ser	Ala	Gly	His	Thr	Glu	
	40					45		*,			50					
ATT G	TT	GAA	TTT	TTG	TTG	CAA	CTT	GGA	GTG	CCA	GTG	AAT	GAT	AAA	GAC	306
Ile V	al	Glu	Phe	Leu	Leu	Gln	Leu	Gly	Val	Pro	Val	Asn	Asp	Lys	Asp	
55					60					65					70	
GAT G	CA	GGT	TGG	TCT	CCT	CTT	CAT	ATT	GCG	GCT	тст	GCT	GGC	CGG	GAT	354
Asp A	la	Gly	Trp	Ser	Pro	Leu	His	Ile	Ala	Ala	Ser	Ala	Gly	Arg	Asp	
				75					80		Y.			85		
GAG A	TT	GTA	AAA	GCC	CTT	CTG	GGA	AAA	GGT	GCT	CAA	GTĠ	TAA	GCT	GTC	402
Glu I	le	Val	Lys	Ala	Leu	Leu	Gly	Lys	Gly	Ala	Gln	Val	Asn	Ala	Val	
			90					95				٠.	100,			
AAT C	AA	AAT	GGC	TGT	ACT	ccc	TTA	CAT	TAT	GCA	GCT	TCG	AAA	AAC	AGG	450
Asn G	ln	Asn	Gly	Cys	Thr	Pro	Leu	His	Tyr	Ala	Ala	Ser	/Lys	Ash	Arg	
		105					110					115				
CAT G	AG	ATC	GCT	GTC	ATG	TTA	CTG	GAA	GGC	GGG	GCT	AAT	CCÀ	GAT	GCT	498
His G	lu	Ile	Ala	Val	Met	Leu	Leu	Glu	Gly	Gly	Ala	Asn	Pro	Asp	Ala \	
1:	20					125					130			\		/

AAG	GAC	CAT	TAT	GAG	GCT	ACA	GCA	ATG	CAC	CGG	GCA	GCA	GCC	AAG	GGT	546
Lys	Asp	His	Tyr	Glu	Ala	Thr	Ala	Met	His	Arg	Ala	Ala	Ala	Lys	${ t Gly}$	
135					140					145					150	
AAC	TTG	AAG	ATG	TTA	CAT	ATC	CTT	CTG	TAC	TAC	AAA	GCA	TCC	ACA	AAC	594
Asn	Leu	Lys	Met	Ile	His	Ile	Leu	Leu	Tyr	Tyr	Lys	Ala	Ser	Thr	Asn	
				155					160					165		
ATC	CAA	GAC	ACT	GAG	GGT	AAC	ACT	CCT	CTA	CAC	TTA	GCC	TGT	GAT	GAG	642
Ile	Gln	Asp	Thr	Glu	${\tt Gly}$	Asn	Thr	Pro	Leu	His	Leu	Ala	Cys	Asp	Glu	
			170					175					180			
GAG	AGA	GTG	GAA	GAA	GCA	AAA	CTG	CTG	GTG	TCC	CAA	GGA	GCA	AGT	ATT	690
Glu	Arg	Val	Glu	Glu	Ala	Lys	Leu	Leu	Val	Ser	Gln	Gly	Ala	Ser	Ile	
		185					190					195				
TAC	ATT	GAG	AAT	AAA	GAA	GAA	AAG	ACA	CCC	CTG	CAA	GTG	GCC	AAA	GGT	738
Tyr	Ile	Glu	Asn	Lys	Glu	Glu	Lys	Thr	Pro	Leu	Gln	Val	Ala	Lys	Gly	
	200					205					210					
GGC	CTG	GGT	TTA	ATA	CTC	AAG	AGA	ATG	GTG	GAA	GGT	TAA	ACA			780
Gly	Leu	Gly	Leu	Ile	Leu	Lys	Arg	Met	Val	Glu	Gly					
215					220					225						

SEQ ID NO: 2

Sequence Length: 226

Sequence Type: Amino acid

Topology: Linear

Molecular Type: Protein

Sequence

Met Glu Gly Cys Val Ser Asn Leu Met Val Cys Asn Leu Ala Tyr Ser 5 10 Gly Lys Leu Glu Glu Leu Lys Glu Ser Ile Leu Ala Asp Lys Ser Leu 25 Ala Thr Arg Thr Asp Gln Asp Ser Arg Thr Ala Leu His Trp Ala Cys 40 Ser Ala Gly His Thr Glu Ile Val Glu Phe Leu Leu Gln Leu Gly Val 55 60 Pro Val Asn Asp Lys Asp Asp Ala Gly Trp Ser Pro Leu His Ile Ala 70 75 Ala Ser Ala Gly Arg Asp Glu Ile Val Lys Ala Leu Leu Gly Lys Gly 85 90

Ala Gln Val Asn Ala Val Asn Gln Asn Gly Cys Thr Pro Leu His Tyr

100 105 110

Ala Ala Ser Lys Asn Arg His Glu Ile Ala Val Met Leu Leu Glu Gl	7
115 120 125	
Gly Ala Asn Pro Asp Ala Lys Asp His Tyr Glu Ala Thr Ala Met His	3
130 135 140	
Arg Ala Ala Lys Gly Asn Leu Lys Met Ile His Ile Leu Leu Ty:	:
145 150 155 166)
Tyr Lys Ala Ser Thr Asn Ile Gln Asp Thr Glu Gly Asn Thr Pro Let	1
165 170 175	
His Leu Ala Cys Asp Glu Glu Arg Val Glu Glu Ala Lys Leu Leu Va	L
180 185 190	
Ser Gln Gly Ala Ser Ile Tyr Ile Glu Asn Lys Glu Glu Lys Thr Pro	>
195 200 205	
Leu Gln Val Ala Lys Gly Gly Leu Gly Leu Ile Leu Lys Arg Met Va	L
210 215 220	
Glu Gly	
225	
SEQ ID NO: 3	
Sequence Length: 693	
Sequence Type: Nucleic acid	
Strandedness: Double	
Topology: Linear	
Molecular Type: cDNA	
Sequence	
ATG GAG GGG TGT GTG TCT AAC ATA ATG ATC TGT AAC CTG GCC TAC AG	r 48
Met Glu Gly Cys Val Ser Asn Ile Met Ile Cys Asn Leu Ala Tyr Se	:
5 10 15	
GGG AAG CTG GAT GAG TTG AAG GAG CGC ATT TTG GCT GAT AAA TCT CTG	96
Gly Lys Leu Asp Glu Leu Lys Glu Arg Ile Leu Ala Asp Lys Ser Leu	1
20 25 30	
GCT ACT AGA ACT GAT CAG GAC AGC AGA ACA GCT TTG CAC TGG GCA TG	144
Ala Thr Arg Thr Asp Gln Asp Ser Arg Thr Ala Leu His Trp Ala Cys	3
35 40 45	

TCA GCT GGC CAT ACA GAA ATT GTT GAA TTC TTG CTG CAA CTT GGA GTG

Ser Ala Gly His Thr Glu Ile Val Glu Phe Leu Leu Gln Leu Gly Val

60

55

50

192

CCA	GTN	AAT	GAT	AAA	GAT	GAC	GCA	GGT	TGG	TCT	CCT	CTT	CAT	ATT	GCT	240
Pro	Val	Asn	Asp	Lys	Asp	Asp	Ala	$\mathtt{Gl}\mathtt{Y}$	Trp	Ser	Pro	Leu	His	Ile	Ala	
65					70					75					80	
GCC	TCC	GCT	GGC	CGG	GAT	GAG	ATT	GTA	AAA	GCC	CTT	CTG	GTG	AAA	GGT	288
Ala	Ser	Ala	Gly	Arg	Asp	Glu	Ile	Val	Lys	Ala	Leu	Leu	Val	Lys	Gly	
				85					90					95		
GCA	CAT	GTT	AAT	TCT	GTC	AAT	CAA	AAC	GGC	TGC	ACT	CCA	CTC	CAT	TAT	336
Ala	His	Val	Asn	Ser	Val	Asn	Gln	Asn	Gly	Суз	Thr	Pro	Leu	His	Tyr	
			100					105					110			
GCA	GCT	TCG	AAG	AAT	AGG	CAT	GAG	ATT	TCT	GTT	ATG	TTA	CTA	GAA	GGT	384
Ala	Ala	Ser	Lys	Asn	Arg	His	Glu	Ile	Ser	Val	Met	Leu	Leu	Glu	Gly	
		115					120					125				
GGG	GCT	AAC	CCA	GAT	GCG	AAG	GAC	CAT	TAC	GAT	GCT	ACA	GCA	ATG	CAC	432
Gly	Ala	Asn	Pro	Asp	Ala	Lys	Asp	His	Tyr	Asp	Ala	Thr	Ala	Met	His	
	130					135					140					
CGG	GCA	GCA	GCC	AAG	GGT	AAC	TTG	AAG	ATG	GTT	CAC	ATC	CTT	CTG	TTC	480
Arg	Ala	Ala	Ala	Lys	Gly	Asn	Leu	Lys	Met	Val	His	Ile	Leu	Leu	Phe	
145					150					155					160	
TAC	AAA	GCA	TCC	ACA	AAC	ATC	CAA	GAC	ACT	GAG	GGT	AAC	ACT	CCT	CTA	528
Tyr	Lys	Ala	Ser	Thr	Asn	Ile	Gln	Asp	Thr	Glu	Gly	Asn	Thr	Pro	Leu	
				165					170					175		
CAC	TTA	GCC	TGT	GAT	GAA	GAG	AGA	GTG	GAA	GAG	GCA	AAA	TTT	CTG	GTG	576
His	Leu	Ala	Cys	Asp	Glu	Glu	Arg	Val	Glu	Glu	Ala	Lys	Phe	Leu	Val	
			180					185					190			
ACT	CAA	GGA	GCA	AGT	ATT	TAC	ATT	GAG	AAT	AAA	GAA	GAA	AAG	ACA	CCC	624
Thr	Gln	Gly	Ala	Ser	Ile	Tyr	Ile	Glu	Asn	Lys	Glu	Glu	Lys	Thr	Pro	
		195					200					205				
CTG	CAA	GTT	GCC	AAA	GGG	GGC	CTG	GGT	TTA	ATA	CTC	AAG	AGA	CTA	GCA	672
Leu	Gln	Val	Ala	Lys	Gly	Gly	Leu	Gly	Leu	Ile	Leu	Lys	Arg	Leu	Ala	
	210					215					220					
GAA	AGT	GAA	GAG	GCT	TCT	ATG	TAG									720
Glu	Ser	Glu	Glu	Ala	Ser	Met										
225					220											

SEQ ID NO: 4

Sequence Length: 231

Sequence Type: Amino acid

Topology: Linear

Molecular Type: Protein

Sequence

Met Glu Gly Cys Val Ser Asn Ile Met Ile Cys Asn Leu Ala Tyr Ser

1 5 10 15

Gly Lys Leu Asp Glu Leu Lys Glu Arg Ile Leu Ala Asp Lys Ser Leu
20 25 30

Ala Thr Arg Thr Asp Gln Asp Ser Arg Thr Ala Leu His Trp Ala Cys
35 40 45

Ser Ala Gly His Thr Glu Ile Val Glu Phe Leu Gln Leu Gly Val
50 55 60

Pro Val Asn Asp Lys Asp Asp Ala Gly Trp Ser Pro Leu His Ile Ala 65 70 75 80

Ala Ser Ala Gly Arg Asp Glu Ile Val Lys Ala Leu Leu Val Lys Gly
85 90 95

Ala His Val Asn Ser Val Asn Gln Asn Gly Cys Thr Pro Leu His Tyr
100 105 110

Ala Ala Ser Lys Asn Arg His Glu Ile Ser Val Met Leu Leu Glu Gly
115 120 125

Gly Ala Asn Pro Asp Ala Lys Asp His Tyr Asp Ala Thr Ala Met His 130 135 140

Arg Ala Ala Lys Gly Asn Leu Lys Met Val His Ile Leu Leu Phe 145 150 155 160

Tyr Lys Ala Ser Thr Asn Ile Gln Asp Thr Glu Gly Asn Thr Pro Leu
165 170 175

His Leu Ala Cys Asp Glu Glu Arg Val Glu Glu Ala Lys Phe Leu Val 180 185 190

Thr Gln Gly Ala Ser Ile Tyr Ile Glu Asn Lys Glu Glu Lys Thr Pro 195 200 205

Leu Gln Val Ala Lys Gly Gly Leu Gly Leu Ile Leu Lys Arg Leu Ala 210 215 220

Glu Ser Glu Glu Ala Ser Met

225 230

SEQ ID NO: 5

Sequence Length: 693

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: cDNA

Sequence ATG GAG GGG TGT GTG TCT AAC CTA ATG GTC TGT AAC CTG GCC TAC AAC 48 Met Glu Gly Cys Val Ser Asn Leu Met Val Cys Asn Leu Ala Tyr Asn GGG AAG CTG GAT GAG TTG AAG GAA AGC ATT TTG GCT GAT AAG TCT CTG 96 Gly Lys Leu Asp Glu Leu Lys Glu Ser Ile Leu Ala Asp Lys Ser Leu 25 30 GCC ACT AGA ACT GAT CAG GAC AGC AGA ACA GCA TTG CAC TGG GCA TGC 144 Ala Thr Arg Thr Asp Gln Asp Ser Arg Thr Ala Leu His Trp Ala Cys 35 TCA GCT GGT CAT ACA GAA ATT GTT GAA TTC TTG CTG CAA CTT GGA GTG 192 Ser Ala Gly His Thr Glu Ile Val Glu Phe Leu Leu Gln Leu Gly Val 50 55 CCA GTA AAT GAA AAA GAC GAT GCA GGT TGG TCT CCT CTT CAT ATT GCT 240 Pro Val Asn Glu Lys Asp Asp Ala Gly Trp Ser Pro Leu His Ile Ala 65 70 75 GCT TCC GCT GGC CGG GAT GAG ATT GTA AAA GCC CTT CTG ATA AAA GGG 288 Ala Ser Ala Gly Arg Asp Glu Ile Val Lys Ala Leu Leu Ile Lys Gly 85 90 95 GCA CAA GTG AAT GCC GTC AAT CAG AAT GGC TGC ACG GCC CTT CAT TAT 336 Ala Gln Val Asp Ala Val Asn Gln Asn Gly Cys Thr Ala Leu His Tyr 100 105 GCA GCT TCC AAG AAT AGG CAT GAG ATT GCT GTT ATG TTA CTA GAA GGT 384 Ala Ser Lys Asn Arg His Glu Ile Ala Val Met Leu Leu Glu Gly GGG GCT AAT CCA GAT GCT AAG AAC CAT TAT GAT GCT ACA GCA ATG CAC 432 Gly Ala Asn Pro Asp Ala Lys Asn His Tyr Asp Ala Thr Ala Met His 130 135 CGG GCA GCC AAG GGT AAC TTG AAG ATG GTT CAT ATC CTT CTG TTC 480 Arg Ala Ala Lys Gly Asn Leu Lys Met Val His Ile Leu Leu Phe 145 150 155 160 TAC AAA GCA TCC ACA AAC ATC CAA GAT ACT GAG GGT AAC ACT CCT CTA 528 Tyr Lys Ala Ser Thr Asn Ile Gln Asp Thr Glu Gly Asn Thr Pro Leu 165 170 CAC TTA GCC TGT GAT GAG GAG AGA GTG GAA GAA GCA AAA TTG CTG GTG 576 His Leu Ala Cys Asp Glu Glu Arg Val Glu Glu Ala Lys Leu Val

185

190

180

ACC	CAA	GGA	GCA	AGT	ATT	TAC	ATT	GAA	AAT	AAG	GAA	GAA	AAG	ACA	CCG	624
Thr	Gln	Gly	Ala	Ser	Ile	Tyr	Ile	Glu	Asn	Lys	Glu	Glu	Lys	Thr	Pro	
		195					200					205				
CTG	CAA	GTC	GCQ	AAA	GGG	GGC	CTG	GGT	TTA	ATA	CTC	AAA	AGA	ATC	GCA	672
Leu	Gln	Val	Ala	Lys	Gly	Gly	Leu	Gly	Leu	Ile	Leu	Lys	Arg	Ile	Ala	
	210			\		215					220					
GAA	AGT	GAA	GAG	g¢ī	TCT	ATG	TAG									720
Glu	Ser	Glu	Glu	Ala	Ser	Met										
225				/	230											
SEQ	ID	NO:	: 6													
Seq	uen	ce I	eng	th:	2/3	31										
Seq	uen	ce 1	уре	: 2	Amir	no a	cid									
Top	olo	gy:	Li	nea	r											
Mol	ecu:	lar	Тур	e:	Pro	oteli	n		•							
Seq	uen	ce				\										
Met	Glu	Gly	Суз	Val	Ser	Asn	Leu	Met	Val	Cys	Asn	Leu	Ala	Tyr	Asn	
1				5					10					15		
Gly	Lys	Leu	Asp 20	Glu	Leu	Lys	Glu	Ser 25	Ile	Leu	Ala	Asp	Lys 30	Ser	Leu	
Ala	Thr	Ara		Asp	Gln	Asp	Ser		Thr	Ala	Leu	His		Ala	Cvs	
		35		F		···	40	,9				45			010	
Ser	Ala		His	Thr	Glu	Ile		\ Glu	Phe	Leu	Leu		Leu	Glv	Val	
	50	•				55					60			3		
Pro	Val	Asn	Glu	Lys	Asp	Asp	Ala	Gly	Trp	Ser	Pro	Leu	His	Ile	Ala	
65					70				,	75					80	
Ala	Ser	Ala	${\tt Gly}$	Arg	Asp	Glu	Ile	Val	Lys	Ala	Leu	Leu	Ile	Lys	Gly	
				85					90/	'				95		
Ala	Gln	Val	Asn	Ala	Val	Asn	Gln	Asn	Gly	Суз	Thr	Ala	Leu	His	Tyr	
			100					105		1			110			
Ala	Ala	Ser	Lys	Asn	Arg	His	Glu	Ile	Ala	Val	Met	Leu	Leu	Glu	Gly	
		115					120			j	`\	125				
Gly		Asn	Pro	Asp	Ala	Lys	Asn	His	Tyr	Asp	Ala	Thr	Ala	Met	His	
	130					135					140					
	Ala	Ala	Ala	Lys	_	Asn	Leu	Lys	Met		His	Ile	Leu	Leu		
145	_				150			_		155	``	_		_	160	
Tyr	Lys	Ala	Ser		Asn	Ile	Gln	Asp	Thr	Glu	Gly	Asn	Thr		Leu	
				165					170					175		

His Leu Ala Cys Asp Glu Glu Arg Val Glu Glu Ala Lys Leu Leu Val

180 185

Thr Gln Gly Ala Ser Ile Tyr Ile Glu Asn Lys Glu Glu Lys Thr Pro

195 200 205

Leu Gln Val Afa Lys Gly Gly Leu Gly Leu Ile Leu Lys Arg Ile Val

210 \ 215 220

230

Glu Ser Glu Glu Ala Ser Met

225

SEQ ID NO: 7

Sequence Length: 15

Sequence Type: Amino acid

Topology: Linear

Molecular Type: Peptide

Sequence

Met Glu Gly Cys Val Ser Asn Leu Met Val Cys Asn Leu Ala Tyr

1 5 \ 10 15

SEQ ID NO: 8

Sequence Length: 20

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

CCTGTCGCT TTACCTCCCCA

SEQ ID NO: 9

Sequence Length: 20

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

TACCTCCCA CACACAGATT

20

20